SEQUENCE LISTING

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Xu, H., Eric

<120> STRUCTURE OF A GLUCOCORTICOID RECEPTOR LIGAND BINDING DOMAIN COMPRISING AND EXPANDED BINDING POCKET AND METHODS EMPLOYING SAME

<130> PU4803

<160> 11

<170> PatentIn version 3.1

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agt gtg ctt gct cag gag agg gga gat gtg atg gac ttc tat aaa acc       96
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
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cta aga gga gga gct act gtg aag gtt tct gcg tct tca ccc tca ctg      144
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gct gtc gct tct caa tca gac tcc aag cag cga aga ctt ttg gtt gat      192
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
    50                  55                  60

ttt cca aaa ggc tca gta agc aat gcg cag cag cca gat ctg tcc aaa      240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65                  70                  75                  80

gca gtt tca ctc tca atg gga ctg tat atg gga gag aca gaa aca aaa      288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
                85                  90                  95

gtg atg gga aat gac ctg gga ttc cca cag cag ggc caa atc agc ctt      336
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
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tcc tcg ggg gaa aca gac tta aag ctt ttg gaa gaa agc att gca aac      384
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
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ctc aat agg tcg acc agt gtt cca gag aac ccc aag agt tca gca tcc      432
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    130                 135                 140

act gct gtg tct gct gcc ccc aca gag aag gag ttt cca aaa act cac      480
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145                 150                 155                 160

tct gat gta tct tca gaa cag caa cat ttg aag ggc cag act ggc acc      528
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
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aac ggt ggc aat gtg aaa ttg tat acc aca gac caa agc acc ttt gac      576
Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
            180                 185                 190

att ttg cag gat ttg gag ttt tct tct ggg tcc cca ggt aaa gag acg      624
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ctt tct cct ctg gcg gga gaa gac gat tca ttc ctt ttg gaa gga aac      720
Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
225                 230                 235                 240

tcg aat gag gac tgc aag cct ctc att tta ccg gac act aaa ccc aaa      768
Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
                245                 250                 255

att aag gat aat gga gat ctg gtt ttg tca agc ccc agt aat gta aca      816
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ctg ccc caa gtg aaa aca gaa aaa gaa gat ttc atc gaa ctc tgc acc      864
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cct ggg gta att aag caa gag aaa ctg ggc aca gtt tac tgt cag gca      912
Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
    290                 295                 300

agc ttt cct gga gca aat ata att ggt aat aaa atg tct gcc att tct      960
Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305                 310                 315                 320

gtt cat ggt gtg agt acc tct gga gga cag atg tac cac tat gac atg     1008
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aat aca gca tcc ctt tct caa cag cag gat cag aag cct att ttt aat     1056
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    370                 375                 380

ggt cga aca gtt ttt tct aat ggc tat tca agc ccc agc atg aga cca     1200
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gat gta agc tct cct cca tcc agc tcc tca aca gca aca aca gga cca     1248
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cct ccc aaa ctc tgc ctg gtg tgc tct gat gaa gct tca gga tgt cat     1296
Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
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Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
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gtg gaa gga cag cac aat tac cta tgt gct gga agg aat gat tgc atc     1392
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atc gat aaa att cga aga aaa aac tgc cca gca tgc cgc tat cga aaa     1440
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465                 470                 475                 480

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                485                 490                 495

ata aaa gga att cag cag gcc act aca gga gtc tca caa gaa acc tct     1536
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tat gca gga tat gat agc tct gtt cca gac tca act tgg agg atc atg      1680
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tgg gca aag gca ata cca ggt ttc agg aac tta cac ctg gat gac caa      1776
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Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
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cct gat ctg att att aat gag cag aga atg act cta ccc tgc atg tac      1920
Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
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gac caa tgt aaa cac atg ctg tat gtt tcc tct gag tta cac agg ctt      1968
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cag gta tct tat gaa gag tat ctc tgt atg aaa acc tta ctg ctt ctc      2016
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tct tca gtt cct aag gac ggt ctg aag agc caa gag cta ttt gat gaa      2064
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gaa gga aac tcc agc cag aac tgg cag cgg ttt tat caa ctg aca aaa      2160
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ctc ttg gat tct atg cat gaa gtg gtt gaa aat ctc ctt aac tat tgc      2208
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ttc caa aca ttt ttg gat aag acc atg agt att gaa ttc ccc gag atg      2256
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            740                 745                 750

tta gct gaa atc atc acc aat cag ata cca aaa tat tca aat gga aat      2304
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atc aaa aaa ctt ctg ttt cat caa aag tga                                  2334
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Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
        35                  40                  45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
    50                  55                  60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65                  70                  75                  80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
                85                  90                  95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
            100                 105                 110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
        115                 120                 125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
    130                 135                 140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
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Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
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Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
            180                 185                 190

Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
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Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
    210                 215                 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
225                 230                 235                 240
Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
                245                 250                 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
            260                 265                 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
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Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
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Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305                 310                 315                 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
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Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
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Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
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Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
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Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
385                 390                 395                 400

Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
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Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
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Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
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Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu
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Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu
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Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met
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Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln
580 585 590

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Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
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Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
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Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu
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Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
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Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys
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Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met
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Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
20 25 30

cta aga gga gga gct act gtg aag gtt tct gcg tct tca ccc tca ctg 144
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35 40 45

gct gtc gct tct caa tca gac tcc aag cag cga aga ctt ttg gtt gat 192
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60

ttt cca aaa ggc tca gta agc aat gcg cag cag cca gat ctg tcc aaa 240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80

gca gtt tca ctc tca atg gga ctg tat atg gga gag aca gaa aca aaa 288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys

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                  85                  90                  95

gtg atg gga aat gac ctg gga ttc cca cag cag ggc caa atc agc ctt      336
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
            100                 105                 110

tcc tcg ggg gaa aca gac tta aag ctt ttg gaa gaa agc att gca aac      384
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
        115                 120                 125

ctc aat agg tcg acc agt gtt cca gag aac ccc aag agt tca gca tcc      432
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
    130                 135                 140

act gct gtg tct gct gcc ccc aca gag aag gag ttt cca aaa act cac      480
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145                 150                 155                 160

tct gat gta tct tca gaa cag caa cat ttg aag ggc cag act ggc acc      528
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
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aac ggt ggc aat gtg aaa ttg tat acc aca gac caa agc acc ttt gac      576
Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
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att ttg cag gat ttg gag ttt tct tct ggg tcc cca ggt aaa gag acg      624
Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
        195                 200                 205

aat gag agt cct tgg aga tca gac ctg ttg ata gat gaa aac tgt ttg      672
Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
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tcg aat gag gac tgc aag cct ctc att tta ccg gac act aaa ccc aaa      768
Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
                245                 250                 255

att aag gat aat gga gat ctg gtt ttg tca agc ccc agt aat gta aca      816
Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
            260                 265                 270

ctg ccc caa gtg aaa aca gaa aaa gaa gat ttc atc gaa ctc tgc acc      864
Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
        275                 280                 285

cct ggg gta att aag caa gag aaa ctg ggc aca gtt tac tgt cag gca      912
Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
    290                 295                 300

agc ttt cct gga gca aat ata att ggt aat aaa atg tct gcc att tct      960
Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305                 310                 315                 320

gtt cat ggt gtg agt acc tct gga gga cag atg tac cac tat gac atg     1008
Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
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aat aca gca tcc ctt tct caa cag cag gat cag aag cct att ttt aat     1056
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gtc att cca cca att ccc gtt ggt tcc gaa aat tgg aat agg tgc caa     1104
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Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
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ggt cga aca gtt ttt tct aat ggc tat tca agc ccc agc atg aga cca     1200
Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
385                 390                 395                 400

gat gta agc tct cct cca tcc agc tcc tca aca gca aca aca gga cca     1248
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cct ccc aaa ctc tgc ctg gtg tgc tct gat gaa gct tca gga tgt cat     1296
Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
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tat gga gtc tta act tgt gga agc tgt aaa gtt ttc ttc aaa aga gca     1344
Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
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gtg gaa gga cag cac aat tac cta tgt gct gga agg aat gat tgc atc     1392
Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
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atc gat aaa att cga aga aaa aac tgc cca gca tgc cgc tat cga aaa     1440
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ata aaa gga att cag cag gcc act aca gga gtc tca caa gaa acc tct     1536
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            500                 505                 510

gaa aat cct ggt aac aaa aca ata gtt cct gca acg tta cca caa ctc     1584
Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu
        515                 520                 525

acc cct acc ctg gtg tca ctg ttg gag gtt att gaa cct gaa gtg tta     1632
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545                 550                 555                 560

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Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
    610                 615                 620

cct gat ctg att att aat gag cag aga atg act cta ccc tgc atg tac     1920
Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
625                 630                 635                 640

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cag gta tct tat gaa gag tat ctc tgt atg aaa acc tta ctg ctt ctc     2016
Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu Leu
            660                 665                 670

tct tca gtt cct aag gac ggt ctg aag agc caa gag cta ttt gat gaa     2064
Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
        675                 680                 685


att aga atg acc tac atc aaa gag cta gga aaa gcc att gtc aag agg     2112
Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg
    690                 695                 700

gaa gga aac tcc agc cag aac tgg cag cgg ttt tat caa ctg aca aaa     2160
Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys
705                 710                 715                 720

ctc ttg gat tct atg cat gaa gtg gtt gaa aat ctc ctt aac tat tgc     2208
Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys
                725                 730                 735

ttc caa aca ttt ttg gat aag acc atg agt att gaa ttc ccc gag atg     2256
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tta gct gaa atc atc acc aat cag ata cca aaa tat tca aat gga aat     2304
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atc aaa aaa ctt ctg ttt cat caa aag tga                             2334
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Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
1               5                  10                  15

Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
            20                  25                  30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
        35                  40                  45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
    50                  55                  60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65                  70                  75                  80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
                85                  90                  95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
            100                 105                 110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
        115                 120                 125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
    130                 135                 140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145                 150                 155                 160

Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
                165                 170                 175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
            180                 185                 190

Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
        195                 200                 205

Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
    210                 215                 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
225                 230                 235                 240
```

```
Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
                245                 250                 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
            260                 265                 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
        275                 280                 285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
    290                 295                 300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305                 310                 315                 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
                325                 330                 335

Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
            340                 345                 350

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
        355                 360                 365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
    370                 375                 380
Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
385                 390                 395                 400

Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
                405                 410                 415

Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
            420                 425                 430

Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
        435                 440                 445

Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
    450                 455                 460

Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys
465                 470                 475                 480

Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys
                485                 490                 495
```

```
Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser
            500                 505                 510

Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu
        515                 520                 525

Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu
    530                 535                 540

Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met
545                 550                 555                 560

Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys
                565                 570                 575

Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln
            580                 585                 590

Met Thr Leu Leu Gln Tyr Ser Trp Met Ser Leu Met Ala Phe Ala Leu
        595                 600                 605

Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
    610                 615                 620

Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
625                 630                 635                 640

Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu
                645                 650                 655
Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu Leu
            660                 665                 670

Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
        675                 680                 685

Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg
    690                 695                 700

Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys
705                 710                 715                 720

Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys
                725                 730                 735

Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met
            740                 745                 750
```

```
Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn
        755                 760                 765

Ile Lys Lys Leu Leu Phe His Gln Lys
    770                 775
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<210> 5

<211> 774

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(771)

<223>

<400> 5

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gtt cct gca acg tta cca caa ctc acc cct acc ctg gtg tca ctg ttg       48
Val Pro Ala Thr Leu Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu
1               5                   10                  15

gag gtt att gaa cct gaa gtg tta tat gca gga tat gat agc tct gtt       96
Glu Val Ile Glu Pro Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val
            20                  25                  30

cca gac tca act tgg agg atc atg act acg ctc aac atg tta gga ggg      144
Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly
        35                  40                  45

cgg caa gtg att gca gca gtg aaa tgg gca aag gca ata cca ggt ttc      192
Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe
    50                  55                  60

agg aac tta cac ctg gat gac caa atg acc cta ctg cag tac tcc tgg      240
Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp
65                  70                  75                  80

atg ttt ctt atg gca ttt gct ctg ggg tgg aga tca tat aga caa tca      288
Met Phe Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser
                85                  90                  95

agt gca aac ctg ctg tgt ttt gct cct gat ctg att att aat gag cag      336
Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln
            100                 105                 110

aga atg act cta ccc tgc atg tac gac caa tgt aaa cac atg ctg tat      384
Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr
        115                 120                 125

gtt tcc tct gag tta cac agg ctt cag gta tct tat gaa gag tat ctc      432
```

```
Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu
    130                 135                 140

tgt atg aaa acc tta ctg ctt ctc tct tca gtt cct aag gac ggt ctg      480
Cys Met Lys Thr Leu Leu Leu Leu Ser Ser Val Pro Lys Asp Gly Leu
145                 150                 155                 160

aag agc caa gag cta ttt gat gaa att aga atg acc tac atc aaa gag      528
Lys Ser Gln Glu Leu Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu
                165                 170                 175

cta gga aaa gcc att gtc aag agg gaa gga aac tcc agc cag aac tgg      576
Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp
            180                 185                 190

cag cgg ttt tat caa ctg aca aaa ctc ttg gat tct atg cat gaa gtg      624
Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Met His Glu Val
        195                 200                 205

gtt gaa aat ctc ctt aac tat tgc ttc caa aca ttt ttg gat aag acc      672
Val Glu Asn Leu Leu Asn Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr
    210                 215                 220

atg agt att gaa ttc ccc gag atg tta gct gaa atc atc acc aat cag      720
Met Ser Ile Glu Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln
225                 230                 235                 240

ata cca aaa tat tca aat gga aat atc aaa aaa ctt ctg ttt cat caa      768
Ile Pro Lys Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln
                245                 250                 255

aag tga                                                             774
Lys
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<210> 6

<211> 257

<212> PRT

<213> Homo sapiens

<400> 6

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Val Pro Ala Thr Leu Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu
1               5                   10                  15

Glu Val Ile Glu Pro Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val
            20                  25                  30

Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly
        35                  40                  45

Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe
    50                  55                  60

Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp
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65 70 75 80

Met Phe Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser
85 90 95

Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln
100 105 110

Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr
115 120 125

Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu
130 135 140

Cys Met Lys Thr Leu Leu Leu Leu Ser Ser Val Pro Lys Asp Gly Leu
145 150 155 160

Lys Ser Gln Glu Leu Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu
165 170 175

Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp
180 185 190

Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Met His Glu Val
195 200 205

Val Glu Asn Leu Leu Asn Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr
210 215 220

Met Ser Ile Glu Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln
225 230 235 240

Ile Pro Lys Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln
245 250 255

Lys

<210> 7

<211> 774

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(771)

<223>

<400> 7

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Val Pro Ala Thr Leu Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu
1               5                   10                  15

gag gtt att gaa cct gaa gtg tta tat gca gga tat gat agc tct gtt       96
Glu Val Ile Glu Pro Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val
            20                  25                  30

cca gac tca act tgg agg atc atg act acg ctc aac atg tta gga ggg      144
Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly
        35                  40                  45

cgg caa gtg att gca gca gtg aaa tgg gca aag gca ata cca ggt ttc      192
Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe
    50                  55                  60

agg aac tta cac ctg gat gac caa atg acc cta ctg cag tac tcc tgg      240
Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp
65                  70                  75                  80

atg tcc ctt atg gca ttt gct ctg ggg tgg aga tca tat aga caa tca      288
Met Ser Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser
                85                  90                  95

agt gca aac ctg ctg tgt ttt gct cct gat ctg att att aat gag cag      336
Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln
            100                 105                 110

aga atg act cta ccc tgc atg tac gac caa tgt aaa cac atg ctg tat      384
Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr
        115                 120                 125

gtt tcc tct gag tta cac agg ctt cag gta tct tat gaa gag tat ctc      432
Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu
    130                 135                 140

tgt atg aaa acc tta ctg ctt ctc tct tca gtt cct aag gac ggt ctg      480
Cys Met Lys Thr Leu Leu Leu Leu Ser Ser Val Pro Lys Asp Gly Leu
145                 150                 155                 160

aag agc caa gag cta ttt gat gaa att aga atg acc tac atc aaa gag      528
Lys Ser Gln Glu Leu Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu
                165                 170                 175

cta gga aaa gcc att gtc aag agg gaa gga aac tcc agc cag aac tgg      576
Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp
            180                 185                 190

cag cgg ttt tat caa ctg aca aaa ctc ttg gat tct atg cat gaa gtg      624
Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Met His Glu Val
        195                 200                 205
```

```
gtt gaa aat ctc ctt aac tat tgc ttc caa aca ttt ttg gat aag acc      672
Val Glu Asn Leu Leu Asn Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr
    210                 215                 220

atg agt att gaa ttc ccc gag atg tta gct gaa atc atc acc aat cag      720
Met Ser Ile Glu Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln
225                 230                 235                 240

ata cca aaa tat tca aat gga aat atc aaa aaa ctt ctg ttt cat caa      768
Ile Pro Lys Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln
                245                 250                 255

aag tga                                                             774
Lys
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<210> 8

<211> 257

<212> PRT

<213> Homo sapiens

<400> 8

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Val Pro Ala Thr Leu Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu
1               5                   10                  15

Glu Val Ile Glu Pro Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val
            20                  25                  30

Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly
        35                  40                  45

Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe
    50                  55                  60

Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp
65                  70                  75                  80

Met Ser Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser
                85                  90                  95

Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln
            100                 105                 110

Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr
        115                 120                 125

Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu
```

130 135 140

Cys Met Lys Thr Leu Leu Leu Leu Ser Ser Val Pro Lys Asp Gly Leu
145 150 155 160

Lys Ser Gln Glu Leu Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu
165 170 175

Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp
180 185 190

Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Met His Glu Val
195 200 205

Val Glu Asn Leu Leu Asn Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr
210 215 220

Met Ser Ile Glu Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln
225 230 235 240

Ile Pro Lys Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln
245 250 255

Lys

<210> 9

<211> 14

<212> PRT

<213> Homo sapiens

<400> 9

Lys Glu Asn Ala Leu Leu Arg Tyr Leu Leu Asp Lys Asp Asp
1 5 10

<210> 10

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(5)

<223> X is any amino acid

<400> 10

Leu Xaa Xaa Leu Leu
1 5

<210> 11

<211> 6

<212> PRT

<213> Homo sapiens

<400> 11

Leu Leu Arg Tyr Leu Leu
1 5